

ACADEMIC RESEARCH LICENSE AGREEMENT

FOR GENEMARK™ SUITE SOFTWARE

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Entire Agreement: The parties hereto acknowledge that each has read this Agreement, understands it, and agrees to be bound by its terms. This Agreement sets forth the entire agreement and understanding between the parties as to the subject matter hereof and merges all prior discussions between them; and neither party shall be bound by any conditions, definitions, warranties, understandings or representations with respect to such subject matter other than as expressly provided herein. This Agreement may not be modified or altered except in writing by an instrument duly executed by authorized officers of both parties. Provided, however, that no provision appearing in any standard form document originated by LICENSEE including, but not limited to, any purchase order or confirmation order, shall be applicable, even if signed by both parties, unless the parties also execute a separate instrument expressly modifying this Agreement to include such provisions as set forth above.

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Please fax the signed agreement to fax: +1 404 603 88 75

EXHIBIT "A"

The GeneMark™ software suite

Description:

GeneMark™ is a genomic data analysis tool designed to predict the presence of protein coding regions in raw DNA sequence text. The program consists of a single executable program (command gm) and several files of parameters that represent the statistical characteristics of known protein coding and non-coding regions of an individual genome. The parameters are encoded in compliance with the EAIFF85 standard, known as IFF.

As an output GeneMark™ generates a PostScript Graphic representation of its analysis, as well as a list of putative protein coding regions, a list of predicted expressed DNA sequences and a list of translated protein sequences (putative proteins or protein fragments).

The user of GeneMark™ should, thereby, be able to locate protein coding regions and annotation the initial DNA sequence.

The GeneMark™ program has several other options that are described in the help message displayed if only the command 'gm' is entered.

Particularly, two important options are: i/ an option for more accurate predicting translations starts in bacterial genes using Ribosomal Binding Site model; ii/ an option for indicating putative frame-shifts (sequencing errors) within predicted coding regions.

The GeneMark suite includes the subsystems that performs the statistical analysis and generates the model parameters, matrices of initial and transition probabilities

Generation of the files of parameters (including Markov model matrices)

MkMat is the software program that produces the GeneMark matrices from the sets of coding and non-coding genomic DNA regions of a given species. The sets are prepared by the user according to the instruction provided with MkMat help file.

Note that some matrices are readily available for download from
<http://opal.biology.gatech.edu/GeneMark/downloads.html>

ViewMat is the software program to view model matrices in readable format. View Mat is also available as a part of the GeneMark suite.

(Although GeneProbe does not take obligation of the SOFTWARE support or maintenance, we will do our best to address your questions, please see <http://www.geneprobe.net/contactus.htm> for faster communication regarding academic distribution use Fax: +1 (404) 603-8875 or e-mail custserv@genepro.com)